



SEQUENCE LISTING

<110> Meares, Claude
Corneillie, Todd
The Regents of the University of California

<120> Multi-Functional Antibodies

<130> 023070-130920US

<140> US 10/631,258

<141> 2003-07-31

<150> US 10/350,555

<151> 2003-01-23

<150> US 10/625,047

<151> 2003-07-22

<160> 72

<170> PatentIn Ver. 2.1

<210> 1

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<212> PRT

<213> Mus musculus

<220>

<223> murine monoclonal antibody 2D12.5 light chain
variable domain (VL)

<400> 1

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			20					25					30		

Asn	Tyr	Ala	Asn	Trp	Val	Gln	Glu	Lys	Pro	Asp	His	Leu	Phe	Thr	Gly
		35					40					45			

Leu	Ile	Gly	Gly	Asn	Asn	Asn	Arg	Pro	Pro	Gly	Val	Pro	Ala	Arg	Phe
	50					55					60				

Ser	Gly	Ser	Leu	Ile	Gly	Asp	Lys	Ala	Ala	Leu	Thr	Ile	Ala	Gly	Thr
65					70					75				80	

Gln	Thr	Glu	Asp	Glu	Ala	Ile	Tyr	Phe	Cys	Ala	Leu	Trp	Tyr	Ser	Asn
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His	Trp	Val	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Thr	Val	Leu	Gly
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<210> 2

<211> 14

<212> PRT

<213> Mus musculus

<220>
 <223> murine monoclonal antibody 2D12.5 light chain
 variable domain (VL) complementarity
 determining region 1 (CDR1)

<400> 2
 Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
 1 5 10

<210> 3
 <211> 7
 <212> PRT
 <213> Mus musculus

<220>
 <223> murine monoclonal antibody 2D12.5 light chain
 variable domain (VL) complementarity
 determining region 2 (CDR2)

<400> 3
 Gly Asn Asn Asn Arg Pro Pro
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<210> 4
 <211> 9
 <212> PRT
 <213> Mus musculus

<220>
 <223> murine monoclonal antibody 2D12.5 light chain
 variable domain (VL) complementarity
 determining region 3 (CDR3)

<400> 4
 Ala Leu Trp Tyr Ser Asn His Trp Val
 1 5

<210> 5
 <211> 119
 <212> PRT
 <213> Mus musculus

<220>
 <223> murine monoclonal antibody 2D12.5 heavy chain
 variable domain (VH)

<400> 5
 Gln Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1 5 10 15
 Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp Tyr
 20 25 30
 Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45
 Gly Val Ile Trp Ser Gly Gly Gly Thr Ala Tyr Thr Ala Ala Phe Ile
 50 55 60

Ser Arg Leu Asn Ile Tyr Lys Asp Asn Ser Lys Asn Gln Val Phe Phe
 65 70 75 80
 Glu Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Met Tyr Tyr Cys Ala
 85 90 95
 Arg Arg Gly Ser Tyr Pro Tyr Asn Tyr Phe Asp Val Trp Gly Gln Gly
 100 105 110
 Thr Thr Val Thr Val Ser Ser
 115

<210> 6
 <211> 5
 <212> PRT
 <213> Mus musculus

<220>
 <223> murine monoclonal antibody 2D12.5 heavy chain
 variable domain (VH) complementarity
 determining region 1 (CDR1)

<400> 6
 Asp Tyr Gly Val His
 1 5

<210> 7
 <211> 16
 <212> PRT
 <213> Mus musculus

<220>
 <223> murine monoclonal antibody 2D12.5 heavy chain
 variable domain (VH) complementarity
 determining region 2 (CDR2)

<400> 7
 Val Ile Trp Ser Gly Gly Gly Thr Ala Tyr Thr Ala Ala Phe Ile Ser
 1 5 10 15

<210> 8
 <211> 11
 <212> PRT
 <213> Mus musculus

<220>
 <223> murine monoclonal antibody 2D12.5 heavy chain
 variable domain (VH) complementarity
 determining region 3 (CDR3)

<400> 8
 Arg Gly Ser Tyr Pro Tyr Asn Tyr Phe Asp Val
 1 5 10

<210> 9
<211> 118
<212> PRT
<213> Mus musculus

<220>
<223> native hybridoma murine 2D12.5 heavy chain
variable region (VH)

<400> 9
Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser
1 5 10 15
Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp Tyr Gly
20 25 30
Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly
35 40 45
Val Ile Trp Ser Gly Gly Gly Thr Ala Tyr Thr Ala Ala Phe Ile Ser
50 55 60
Arg Leu Asn Ile Tyr Lys Asp Asn Ser Lys Asn Gln Val Phe Phe Glu
65 70 75 80
Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Met Tyr Tyr Cys Ala Arg
85 90 95
Arg Gly Ser Tyr Pro Tyr Asn Tyr Phe Asp Val Trp Gly Gln Gly Thr
100 105 110
Thr Val Thr Val Ser Ser
115

<210> 10
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:native cloned
hybridoma murine 2D12.5 heavy chain variable
region (VH)

<400> 10
Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser
1 5 10 15
Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp Tyr Gly
20 25 30
Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly
35 40 45
Val Ile Trp Ser Gly Gly Gly Thr Ala Tyr Thr Ala Ala Phe Ile Ser
50 55 60
Arg Leu Asn Ile Tyr Lys Asp Asn Ser Lys Asn Gln Val Phe Phe Glu
65 70 75 80

Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Met Tyr Tyr Cys Ala Arg
85 90 95

Arg Gly Ser Tyr Pro Tyr Asn Tyr Phe Asp Val Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ala
115

<210> 11
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:N87D cloned
mutant murine 2D12.5 heavy chain variable region
(VH)

<400> 11
Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser
1 5 10 15
Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp Tyr Gly
20 25 30
Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly
35 40 45
Val Ile Trp Ser Gly Gly Gly Thr Ala Tyr Thr Ala Ala Phe Ile Ser
50 55 60
Arg Leu Asn Ile Tyr Lys Asp Asn Ser Lys Asn Gln Val Phe Phe Glu
65 70 75 80
Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg
85 90 95
Arg Gly Ser Tyr Pro Tyr Asn Tyr Phe Asp Val Trp Gly Gln Gly Thr
100 105 110
Thr Val Thr Val Ser Ala
115

<210> 12
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:N87D G53C
cloned mutant murine 2D12.5 heavy chain variable
region (VH)

<400> 12
Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser
1 5 10 15

Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp Tyr Gly
 20 25 30
 Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly
 35 40 45
 Val Ile Trp Ser Cys Gly Gly Thr Ala Tyr Thr Ala Ala Phe Ile Ser
 50 55 60
 Arg Leu Asn Ile Tyr Lys Asp Asn Ser Lys Asn Gln Val Phe Phe Glu
 65 70 75 80
 Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg
 85 90 95
 Arg Gly Ser Tyr Pro Tyr Asn Tyr Phe Asp Val Trp Gly Gln Gly Thr
 100 105 110
 Thr Val Thr Val Ser Ala
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<210> 13
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:N87D G54C
 cloned mutant murine 2D12.5 heavy chain variable
 region (VH)

<400> 13
 Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser
 1 5 10 15
 Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp Tyr Gly
 20 25 30
 Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly
 35 40 45
 Val Ile Trp Ser Gly Cys Gly Thr Ala Tyr Thr Ala Ala Phe Ile Ser
 50 55 60
 Arg Leu Asn Ile Tyr Lys Asp Asn Ser Lys Asn Gln Val Phe Phe Glu
 65 70 75 80
 Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg
 85 90 95
 Arg Gly Ser Tyr Pro Tyr Asn Tyr Phe Asp Val Trp Gly Gln Gly Thr
 100 105 110
 Thr Val Thr Val Ser Ala
 115

<210> 14
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:N87D G55C
 cloned mutant murine 2D12.5 heavy chain variable
 region (VH)

<400> 14
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 1 5 10 15
 Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp Tyr Gly
 20 25 30
 Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly
 35 40 45
 Val Ile Trp Ser Gly Gly Cys Thr Ala Tyr Thr Ala Ala Phe Ile Ser
 50 55 60
 Arg Leu Asn Ile Tyr Lys Asp Asn Ser Lys Asn Gln Val Phe Phe Glu
 65 70 75 80
 Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg
 85 90 95
 Arg Gly Ser Tyr Pro Tyr Asn Tyr Phe Asp Val Trp Gly Gln Gly Thr
 100 105 110
 Thr Val Thr Val Ser Ala
 115

<210> 15
 <211> 354
 <212> DNA
 <213> Mus musculus

<220>
 <223> native hybridoma murine 2D12.5 heavy chain
 variable region (VH)

<400> 15
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 tgcacgggtct ctggtttctc attaactgac tatggtgtac actgggttcg ccagtctcca 120
 ggaaagggtc tggaatggct gggagtgata tggagtgggtg gaggcacggc ctatactgcg 180
 gcgttcatat ccagactgaa catctacaag gacaattcca agaaccaagt tttctttgaa 240
 atgaacagtc tgcaagctaa tgacacagcc atgtattact gtgccagaag gggtagctac 300
 ccttacaact acttcgatgt ctgggggcaa gggaccacag tcaccgtctc ctca 354

<210> 16
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:native cloned
 hybridoma murine 2D12.5 heavy chain variable
 region (VH)

<400> 16
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 tgcacgggtct ctggtttctc attaactgac tatggtgtac actgggttcg ccagtctcca 120
 ggaaagggtc tggaatggct gggagtgata tggagtgggtg gaggcacggc ctatactgcg 180
 gcgttcatat ccagactgaa catctacaag gacaattcca agaaccaagt tttctttgaa 240
 atgaacagtc tgcaagctaa tgacacagcc atgtattact gtgccagaag gggtagctac 300
 cttacaact acttcgatgt ctggggccaa gggaccacgg tcaccgtctc cgca 354

<210> 17
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:N87D cloned
 mutant murine 2D12.5 heavy chain variable region
 (VH)

<400> 17
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 tgcacgggtct ctggtttctc attaactgac tatggtgtac actgggttcg ccagtctcca 120
 ggaaagggtc tggaatggct gggagtgata tggagtgggtg gaggcacggc ctatactgcg 180
 gcgttcatat ccagactgaa catctacaag gacaattcca agaaccaagt tttctttgaa 240
 atgaacagtc tgcaagctga tgacacagcc atgtattact gtgccagaag gggtagctac 300
 cttacaact acttcgatgt ctggggccaa gggaccacgg tcaccgtctc cgca 354

<210> 18
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:N87D G53C
 cloned mutant murine 2D12.5 heavy chain variable
 region (VH)

<400> 18
 gtgaagctgc aggagtctgg acctggccta gtgcagccct cacagagcct gtccatcacc 60
 tgcacgggtct ctggtttctc attaactgac tatggtgtac actgggttcg ccagtctcca 120
 ggaaagggtc tggaatggct gggagtgata tggagtgtgt gaggcacggc ctatactgcg 180
 gcgttcatat ccagactgaa catctacaag gacaattcca agaaccaagt tttctttgaa 240
 atgaacagtc tgcaagctga tgacacagcc atgtattact gtgccagaag gggtagctac 300
 cttacaact acttcgatgt ctggggccaa gggaccacgg tcaccgtctc cgca 354

<210> 19
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:N87D G54C
 cloned mutant murine 2D12.5 heavy chain variable
 region (VH)

<400> 19
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 tgcacgggtct ctggtttctc attaactgac tatggtgtac actgggttcg ccagtctcca 120
 ggaaagggtc tggaatggct gggagtgata tggagtgggt gtggcacggc ctatactgcg 180
 gcgttcatat ccagactgaa catctacaag gacaattcca agaaccaagt tttctttgaa 240
 atgaacagtc tgcaagctga tgacacagcc atgtattact gtgccagaag gggtagctac 300
 ccttacaact acttcgatgt ctgggggcca gggaccacgg tcaccgtctc cgca 354

<210> 20
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:N87D G55C
 cloned mutant murine 2D12.5 heavy chain variable
 region (VH)

<400> 20
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 tgcacgggtct ctggtttctc attaactgac tatggtgtac actgggttcg ccagtctcca 120
 ggaaagggtc tggaatggct gggagtgata tggagtgggt gatgcacggc ctatactgcg 180
 gcgttcatat ccagactgaa catctacaag gacaattcca agaaccaagt tttctttgaa 240
 atgaacagtc tgcaagctga tgacacagcc atgtattact gtgccagaag gggtagctac 300
 ccttacaact acttcgatgt ctgggggcca gggaccacgg tcaccgtctc cgca 354

<210> 21
 <211> 109
 <212> PRT
 <213> Mus musculus

<220>
 <223> native hybridoma murine 2D12.5 light chain
 variable region (VL)

<400> 21
 Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu Thr
 1 5 10 15
 Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn
 20 25 30
 Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly Leu
 35 40 45
 Ile Gly Gly Asn Asn Asn Arg Pro Pro Gly Val Pro Ala Arg Phe Ser
 50 55 60
 Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Ala Gly Thr Gln
 65 70 75 80
 Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Ser Asn His
 85 90 95
 Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly
 100 105

<210> 22
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:native cloned
 hybridoma murine 2D12.5 light chain variable
 region (VL)

<400> 22
 Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu Thr
 1 5 10 15
 Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn
 20 25 30
 Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly Leu
 35 40 45
 Ile Gly Gly Asn Asn Asn Arg Pro Pro Gly Val Pro Ala Arg Phe Ser
 50 55 60
 Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Ala Gly Thr Gln
 65 70 75 80
 Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Ser Asn His
 85 90 95
 Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser
 100 105

<210> 23
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:N53C cloned
 mutant murine 2D12.5 light chain variable region
 (VL)

<400> 23
 Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu Thr
 1 5 10 15
 Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn
 20 25 30
 Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly Leu
 35 40 45
 Ile Gly Gly Cys Asn Asn Arg Pro Pro Gly Val Pro Ala Arg Phe Ser
 50 55 60
 Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Ala Gly Thr Gln
 65 70 75 80

Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Ser Asn His
85 90 95

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser
100 105

<210> 24
<211> 327
<212> DNA
<213> Mus musculus

<220>
<223> native hybridoma murine 2D12.5 light chain
variable region (VL)

<400> 24
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tgtcgctcaa gtactggggc tggtacgact agtaactatg ccaactgggt ccaagagaaa 120
ccagatcatt tattcactgg tctaataagg ggtaataata accgacctcc aggtgttcct 180
gccagattct caggctccct gattggagac aaggctgccc tcaccatcgc agggacacag 240
actgaggatg aggcaatata tttctgtgct ctatggtaca gcaaccattg ggtgttcggt 300
ggaggaacca gactgactgt cctagggc 327

<210> 25
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:native cloned
hybridoma murine 2D12.5 light chain variable
region (VL)

<400> 25
gctgttgatga ctcaggaatc tgcactcacc acatcacctg gtgaaacagt cacactcact 60
tgtcgctcaa gtactggggc tggtacgact agtaactatg ccaactgggt ccaagagaaa 120
ccagatcatt tattcactgg tctaataagg ggtaataata accgacctcc aggtgttcct 180
gccagattct caggctccct gattggagac aaggctgccc tcaccatcgc agggacacag 240
actgaggatg aggcaatata tttctgtgct ctatggtaca gcaaccattg ggtgttcggt 300
gggggaacca aactgactgt cctaagc 327

<210> 26
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:N53C cloned
mutant murine 2D12.5 light chain variable region
(VL)

<400> 26
gctgttgatga ctcaggaatc tgcactcacc acatcacctg gtgaaacagt cacactcact 60
tgtcgctcaa gtactggggc tggtacgact agtaactatg ccaactgggt ccaagagaaa 120
ccagatcatt tattcactgg tctaataagg ggttgtaata accgacctcc aggtgttcct 180
gccagattct caggctccct gattggagac aaggctgccc tcaccatcgc agggacacag 240
actgaggatg aggcaatata tttctgtgct ctatggtaca gcaaccattg ggtgttcggt 300
gggggaacca aactgactgt cctaagc 327

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<210> 27
<211> 218
<212> PRT
<213> Artificial Sequence
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<220>

<223> Description of Artificial Sequence:native cloned chimeric murine 2D12.5 light chain variable region (VL) fused to human anti-tetanus toxin antibody kappa light chain constant region (TTCL)

<400> 27

Arg Ser Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly
1 5 10 15

Glu Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr
20 25 30

Ser Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr
35 40 45

Gly Leu Ile Gly Gly Asn Asn Asn Arg Pro Pro Gly Val Pro Ala Arg
50 55 60

Phe Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Ala Gly
65 70 75 80

Thr Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Ser
85 90 95

Asn His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Arg
100 105 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Leu Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 28

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:N53C cloned
mutant chimeric murine 2D12.5 light chain variable
region (VL) fused to human anti-tetanus toxin
antibody kappa light chain constant region (TTCL)

<400> 28

Arg	Ser	Ala	Val	Val	Thr	Gln	Glu	Ser	Ala	Leu	Thr	Thr	Ser	Pro	Gly	
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Glu	Thr	Val	Thr	Leu	Thr	Cys	Arg	Ser	Ser	Thr	Gly	Ala	Val	Thr	Thr	
			20					25					30			
Ser	Asn	Tyr	Ala	Asn	Trp	Val	Gln	Glu	Lys	Pro	Asp	His	Leu	Phe	Thr	
		35					40					45				
Gly	Leu	Ile	Gly	Gly	Cys	Asn	Asn	Arg	Pro	Pro	Gly	Val	Pro	Ala	Arg	
	50					55					60					
Phe	Ser	Gly	Ser	Leu	Ile	Gly	Asp	Lys	Ala	Ala	Leu	Thr	Ile	Ala	Gly	
65					70				75						80	
Thr	Gln	Thr	Glu	Asp	Glu	Ala	Ile	Tyr	Phe	Cys	Ala	Leu	Trp	Tyr	Ser	
				85					90					95		
Asn	His	Trp	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Ser	Arg	
			100					105					110			
Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	
		115					120					125				
Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	
	130					135					140					
Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	
145					150					155					160	
Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	
			165					170						175		
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	
			180					185					190			
His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Leu	Pro	
		195					200					205				
Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys							
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<210> 29

<211> 109

<212> PRT

<213> Mus musculus

<220>

<223> native hybridoma murine 2D12.5 light chain
variable region (VL)

<400> 29
Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu Thr
1 5 10 15
Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn
20 25 30
Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly Leu
35 40 45
Ile Gly Gly Asn Asn Asn Arg Pro Pro Gly Val Pro Ala Arg Phe Ser
50 55 60
Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Ala Gly Thr Gln
65 70 75 80
Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Ser Asn His
85 90 95
Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly
100 105

<210> 30
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<223> human. anti-tetanus toxin antibody kappa light
chain constant region (TTCL) template

<400> 30
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Leu
85 90 95
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 31
<211> 664
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:native cloned
chimeric murine 2D12.5 light chain variable region
(VL) fused to human anti-tetanus toxin antibody
kappa light chain constant region (TTCL)

<400> 31

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agatctgctg ttgtgactca ggaatctgca ctcaccacat cacctgggtga aacagtcaca 60
ctcacttgctc gctcaagtac tggggctggt acgactagta actatgccaa ctgggtccaa 120
gagaaaccag atcattttatt cactggtcta ataggtggta ataataaccg acctccaggt 180
gttcctgcca gattctcagg ctccctgatt ggagacaagg ctgccctcac catcgcaggg 240
acacagactg aggatgaggc aatatatttc tgtgctctat ggtacagcaa ccattgggtg 300
ttcgggtgggg gaaccaaact gactgtccta agccgaactg tggctgcacc atctgtcttc 360
atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
aataacttct atcccagaga ggccaaagta cagtgggaagg tggataacgc cctccaatcg 480
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600
acctatcagg gcctgagctt gcccgtcaca aagagcttca acaggggaga gtgttaattc 660
taga
```

<210> 32

<211> 664

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:N53C cloned
mutant chimeric murine 2D12.5 light chain variable
region (VL) fused to human anti-tetanus toxin
antibody kappa light chain constant region (TTCL)

<400> 32

```
agatctgctg ttgtgactca ggaatctgca ctcaccacat cacctgggtga aacagtcaca 60
ctcacttgctc gctcaagtac tggggctggt acgactagta actatgccaa ctgggtccaa 120
gagaaaccag atcattttatt cactggtcta ataggtgggt gtaataaccg acctccaggt 180
gttcctgcca gattctcagg ctccctgatt ggagacaagg ctgccctcac catcgcaggg 240
acacagactg aggatgaggc aatatatttc tgtgctctat ggtacagcaa ccattgggtg 300
ttcgggtgggg gaaccaaact gactgtccta agccgaactg tggctgcacc atctgtcttc 360
atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420
aataacttct atcccagaga ggccaaagta cagtgggaagg tggataacgc cctccaatcg 480
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540
agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600
acctatcagg gtctgagctt gcccgtcaca aagagcttca acaggggaga gtgttaattc 660
taga
```

<210> 33

<211> 327

<212> DNA

<213> Mus musculus

<220>

<223> native hybridoma murine 2D12.5 light chain
variable region (VL)

<400> 33

```
gctgttggtga ctcaggaatc tgcactcacc acatcacctg gtgaaacagt cacactcact 60
tgctcgctcaa gtactggggc tggttacgact agtaactatg ccaactgggt ccaagagaaa 120
ccagatcatt tattcactgg tctaataagg gttaataata accgacctcc aggtgttcct 180
gccagattct caggctccct gattggagac aaggctgccc tcaccatcgc agggacacag 240
```

actgaggatg aggcaatata tttctgtgct ctatggtaca gcaaccattg ggtgttcggt 300
ggaggaacca gactgactgt cctaggc 327

<210> 34
<211> 322
<212> DNA
<213> Homo sapiens

<220>
<223> human anti-tetanus toxin antibody kappa light
chain constant region (TTCL) template

<400> 34
cgaactgtgg ctgcaccatc tgtcttcac tccccgccat ctgatgagca gttgaaatct 60
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 120
tggaagggtg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 180
agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag 240
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagcttgcc cgtcacaaag 300
agcttcaaca ggggagagtg tt 322

<210> 35
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:native cloned
chimeric murine 2D12.5 heavy chain variable region
(VH) fused to human anti-tetanus toxin antibody
CH1 heavy chain constant region (TTCH)

<400> 35
Arg Ser Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser
1 5 10 15
Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp
20 25 30
Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp
35 40 45
Leu Gly Val Ile Trp Ser Gly Gly Gly Thr Ala Tyr Thr Ala Ala Phe
50 55 60
Ile Ser Arg Leu Asn Ile Tyr Lys Asp Asn Ser Lys Asn Gln Val Phe
65 70 75 80
Phe Glu Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Arg Gly Ser Tyr Pro Tyr Asn Tyr Phe Asp Val Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val
115 120 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Ser Arg
 225

<210> 36
 <211> 227
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:N87D cloned
 mutant chimeric murine 2D12.5 heavy chain variable
 region (VH) fused to human anti-tetanus toxin
 antibody CH1 heavy chain constant region (TTCH)

<400> 36
 Arg Ser Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser
 1 5 10 15
 Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp
 20 25 30
 Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp
 35 40 45
 Leu Gly Val Ile Trp Ser Gly Gly Gly Thr Ala Tyr Thr Ala Ala Phe
 50 55 60
 Ile Ser Arg Leu Asn Ile Tyr Lys Asp Asn Ser Lys Asn Gln Val Phe
 65 70 75 80
 Phe Glu Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Arg Gly Ser Tyr Pro Tyr Asn Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Ser Arg
 225

<210> 38
 <211> 227
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:N87D G54C
 cloned mutant chimeric murine 2D12.5 heavy chain
 variable region (VH) fused to human anti-tetanus
 toxin antibody CH1 heavy chain constant region
 (TTCH)

<400> 38
 Arg Ser Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser
 1 5 10 15
 Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp
 20 25 30
 Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp
 35 40 45
 Leu Gly Val Ile Trp Ser Gly Cys Gly Thr Ala Tyr Thr Ala Ala Phe
 50 55 60
 Ile Ser Arg Leu Asn Ile Tyr Lys Asp Asn Ser Lys Asn Gln Val Phe
 65 70 75 80
 Phe Glu Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Arg Gly Ser Tyr Pro Tyr Asn Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp
210 215 220

Lys Ser Arg
225

<210> 39
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:N87D G55C
cloned mutant chimeric murine 2D12.5 heavy chain
variable region (VH) fused to human anti-tetanus
toxin antibody CH1 heavy chain constant region
(TTCH)

<400> 39
Arg Ser Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser
1 5 10 15
Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp
20 25 30
Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp
35 40 45
Leu Gly Val Ile Trp Ser Gly Gly Cys Thr Ala Tyr Thr Ala Ala Phe
50 55 60
Ile Ser Arg Leu Asn Ile Tyr Lys Asp Asn Ser Lys Asn Gln Val Phe
65 70 75 80
Phe Glu Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg Arg Gly Ser Tyr Pro Tyr Asn Tyr Phe Asp Val Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val
115 120 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Ser Arg
 225

<210> 40
 <211> 227
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:chimeric murine
 2D12.5 heavy chain variable region (VH) fused to
 human anti-tetanus toxin antibody CH1 heavy chain
 constant region (TTCH) expected sequence

<400> 40
 Arg Ser Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser
 1 5 10 15
 Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp
 20 25 30
 Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp
 35 40 45
 Leu Gly Val Ile Trp Ser Gly Gly Gly Thr Ala Tyr Thr Ala Ala Phe
 50 55 60
 Ile Ser Arg Leu Asn Ile Tyr Lys Asp Asn Ser Lys Asn Gln Val Phe
 65 70 75 80
 Phe Glu Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Arg Gly Ser Tyr Pro Tyr Asn Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Ser Arg
 225

<210> 41
 <211> 118
 <212> PRT
 <213> Mus musculus

<220>
 <223> native hybridoma murine 2D12.5 heavy chain
 variable region (VH)

<400> 41
 Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser
 1 5 10 15
 Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asp Tyr Gly
 20 25 30
 Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly
 35 40 45
 Val Ile Trp Ser Gly Gly Gly Thr Ala Tyr Thr Ala Ala Phe Ile Ser
 50 55 60
 Arg Leu Asn Ile Tyr Lys Asp Asn Ser Lys Asn Gln Val Phe Phe Glu
 65 70 75 80
 Met Asn Ser Leu Gln Ala Asn Asp Thr Ala Met Tyr Tyr Cys Ala Arg
 85 90 95
 Arg Gly Ser Tyr Pro Tyr Asn Tyr Phe Asp Val Trp Gly Gln Gly Thr
 100 105 110
 Thr Val Thr Val Ser Ser
 115

<210> 42
 <211> 681
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:native cloned
 chimeric murine 2D12.5 heavy chain variable region
 (VH) fused to human anti-tetanus toxin antibody
 CH1 heavy chain constant region (TTCH)

<400> 42
 agatctgtga agctgcagga gtctggacct ggcctagtgc agccctcaca gagcctgtcc 60
 atcacctgca cgggtctctgg tttctcatta actgactatg gtgtacactg ggttcgccag 120
 tctccaggaa aggggtctgga atggctggga gtgatatgga gtgggtggagg cacggcctat 180
 actgcggcgt tcatatccag actgaacatc tacaaggaca attccaagaa ccaagttttc 240
 tttgaaatga acagtctgca agctaatac acagccatgt attactgtgc cagaaggggt 300
 agctaccctt acaactactt cgatgtctgg ggccaaggga ccacggtcac cgtctccgca 360
 gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420

```

ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtct 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agcagagccc 660
aaatcttgtg acaaatctag a                                     681

```

```

<210> 43
<211> 681
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:N87D cloned
mutant chimeric murine 2D12.5 heavy chain variable
region (VH) fused to human anti-tetanus toxin
antibody CH1 heavy chain constant region (TTCH)

```

```

<400> 43
agatctgtga agctgcagga gtctggacct ggcctagtgc agccctcaca gagcctgtcc 60
atcacctgca cggctctctgg tttctcatta actgactatg gtgtacactg ggttcgccag 120
tctccaggaa agggctctgga atggctggga gtgatatgga gtgggtggagg cacggcctat 180
actgcggcgt tcatatccag actgaacatc tacaaggaca attccaagaa ccaagttttc 240
tttgaaatga acagtctgca agctgatgac acagccatgt attactgtgc cagaaggggt 300
agctaccctt acaactactt cgatgtctgg ggccaaggga ccacggtcac cgtctccgca 360
gcctccacca agggcccacg ggtcttcccc ctggcacccct cctccaagag cacctctggg 420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtct 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agcagagccc 660
aaatcttgtg acaaatctag a                                     681

```

```

<210> 44
<211> 681
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:N87D G53C
cloned mutant chimeric murine 2D12.5 heavy chain
variable region (VH) fused to human anti-tetanus
toxin antibody CH1 heavy chain constant region
(TTCH)

```

```

<400> 44
agatctgtga agctgcagga gtctggacct ggcctagtgc agccctcaca gagcctgtcc 60
atcacctgca cggctctctgg tttctcatta actgactatg gtgtacactg ggttcgccag 120
tctccaggaa agggctctgga atggctggga gtgatatgga gttgtggagg cacggcctat 180
actgcggcgt tcatatccag actgaacatc tacaaggaca attccaagaa ccaagttttc 240
tttgaaatga acagtctgca agctgatgac acagccatgt attactgtgc cagaaggggt 300
agctaccctt acaactactt cgatgtctgg ggccaaggga ccacggtcac cgtctccgca 360
gcctccacca agggcccacg ggtcttcccc ctggcacccct cctccaagag cacctctggg 420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtct 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agcagagccc 660
aaatcttgtg acaaatctag a                                     681

```

<210> 45
<211> 681
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:N87D G54C
cloned mutant chimeric murine 2D12.5 heavy chain
variable region (VH) fused to human anti-tetanus
toxin antibody CH1 heavy chain constant region
(TTCH)

<400> 45

```
agatctgtga agctgcagga gtctgggcct ggcctagtgc agccctcaca gagcctgtcc 60
atcacctgca cggctctctgg tttctcatta actgactatg gtgtacactg gggtcgccag 120
tctccaggaa aggggtctgga atggctggga gtgatatgga gtgggtgtgg cacggcctat 180
actgcggcgt tcatatccag actgaacatc tacaaggaca attccaagaa ccaagttttc 240
tttgaaatga acagtctgca agctgatgac acagccatgt attactgtgc cagaaggggt 300
agctaccctt acaactactt cgatgtcttg ggccaaggga ccacgggtcac cgtctccgca 360
gcctccacca agggcccata ggtcttcccc ctggcaccct cctccaagag cacctctggg 420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtct 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agcagagccc 660
aaatcttgtg acaaactctag a                                     681
```

<210> 46
<211> 681
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:N87D G55C
cloned mutant chimeric murine 2D12.5 heavy chain
variable region (VH) fused to human anti-tetanus
toxin antibody CH1 heavy chain constant region
(TTCH)

<400> 46

```
agatctgtga agctgcagga gtctggacct ggcctagtgc agccctcaca gagcctgtcc 60
atcacctgca cggctctctgg tttctcatta actgactatg gtgtacactg gggtcgccag 120
tctccaggaa aggggtctgga atggctggga gtgatatgga gtgggtggatg cacggcctat 180
actgcggcgt tcatatccag actgaacatc tacaaggaca attccaagaa ccaagttttc 240
tttgaaatga acagtctgca agctgatgac acagccatgt attactgtgc cagaaggggt 300
agctaccctt acaactactt cgatgtcttg ggccaaggga ccacgggtcac cgtctccgca 360
gcctccacca agggcccata ggtcttcccc ctggcaccct cctccaagag cacctctggg 420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtct 480
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agcagagccc 660
aaatcttgtg acaaactctag a                                     681
```

<210> 47
<211> 681
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimeric murine
2D12.5 heavy chain variable region (VH) fused to
human anti-tetanus toxin antibody CH1 heavy chain
constant region (TTCH) expected sequence

<400> 47

```
agatctgtga agctgcagga gtctggacct ggcctagtgc agccctcaca gagcctgtcc 60
atcacctgca cggctctctgg tttctcatta actgactatg gtgtacactg ggttcgccag 120
tctccaggaa agggctctgga atggctggga gtgatatgga gtggtggagg cacggcctat 180
actgcggcgt tcatatccag actgaacatc tacaaggaca attccaagaa ccaagttttc 240
tttgaaatga acagtctgca agctaataac acagccatgt attactgtgc cagaaggggt 300
agctaccctt acaactactt cgatgtctgg ggccaaggga ccacgggtcac cgtctccgca 360
gcctccacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 420
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggg gacgggtgtc 480
tggaactcag gcgccttgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 540
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc 600
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agcagagccc 660
aaatcttgtg acaaactctag a                                     681
```

<210> 48

<211> 354

<212> DNA

<213> Mus musculus

<220>

<223> native hybridoma murine 2D12.5 heavy chain
variable region (VH)

<400> 48

```
gtgaagctgc aggagtcagg acctggccta gtgcagccct cacagagcct gtccatcacc 60
tgcacgggtct ctggtttctc attaactgac tatggtgtac actgggttcg ccagtctcca 120
ggaaagggtc tggaatggct gggagtgata tggagtgggt gaggcacggc ctatactgcg 180
gcgttcatat ccagactgaa catctacaag gacaattcca agaaccaagt tttctttgaa 240
atgaacagtc tgcaagctaa tgacacagcc atgtattact gtgccagaag gggtagctac 300
ccttacaact acttcgatgt ctgggggcca gggaccacag tcaccgtctc ctca      354
```

<210> 49

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:VH2D5' BglII
primer

<400> 49

```
gaagatctgt gaagctgcag gagtctggac c                                     31
```

<210> 50

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:CHTT2DMi primer

<400> 50
 ccacgggtcac cgtctccgca gcctccacca agggc 35

<210> 51
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:VH2DTTmi primer

<400> 51
 gcccttggtg gaggctgcgg agacgggtgac cgtgg 35

<210> 52
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:TTCH3' Xba
 primer

<400> 52
 cgatctagat ttgtcacaag atttgggctc tgc 33

<210> 53
 <211> 140
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:heavy chain
 chimeric construct PCR reaction MT-VENT

<220>
 <221> CDS
 <222> (81)..(134)
 <223> BiP signal sequence

<400> 53
 gccaatgtgc atcagttgtg gtcagcagca aaatcaagtg aatcatctca gtgcaactaa 60
 agggggggatc cgatctcaat atg aag tta tgc ata tta ctg gcc gtc gtc gcc 113
 Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala
 1 5 10

ttt gtt ggc ctc tcg ctc ggg agatct 140
 Phe Val Gly Leu Ser Leu Gly
 15

<210> 54
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:BiP signal
 sequence

<400> 54
 Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala Phe Val Gly Leu Ser
 1 5 10 15

Leu Gly

<210> 55
 <211> 140
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:heavy chain
 chimeric construct PCR reaction MT-VENT

<220>
 <221> CDS
 <222> (19)..(90)
 <223> V5 epitope and polyhistidine region

<400> 55
 tctagagggc ccttcgaa ggt aag cct atc cct aac cct ctc ctc ggt ctc 51
 Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu
 1 5 10
 gat tct acg cgt acc ggt cat cat cac cat cac cat tga gtttaaacc 100
 Asp Ser Thr Arg Thr Gly His His His His His His
 15 20
 gctgatcagc ctcgactgtg ccttctaagg cctgagctcg 140

<210> 56
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:V5 epitope
 and polyhistidine region

<400> 56
 Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr
 1 5 10 15
 Gly His His His His His His
 20

<210> 57
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:MTforward
 sequencing primer

 <400> 57
 catctcagtg caactaaa 18

<210> 58
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:2dvhN87D_pMTBip
 primer

 <400> 58
 catggctgtg tcatcagctt gcagactggt c 31

<210> 59
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:G53C noncoding
 2dG53c_pMT primer

 <400> 59
 cgtgcctcca caactccata tcac 24

<210> 60
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:G54C noncoding
 2dG54c_pMT primer

 <400> 60
 ccgtgccaca accactccat atc 23

<210> 61
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:G55C noncoding
 2dG55c_pMT primer

 <400> 61
 ccgtgcatcc accactccat atc 23

<210> 62
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial
 Sequence:2dvhKBglII_pMTBip primer

 <400> 62
 gctcgggaga tgtgtgaagc tg 22

 <210> 63
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:BGHreverse
 sequencing primer

 <400> 63
 tagaaggcac agtcgagg 18

 <210> 64
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:2dVL5'Bgl
 primer

 <400> 64
 gaagatctgc tgttgtgact caggaatct 29

 <210> 65
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:2dVLMiTop
 primer

 <400> 65
 accaaactga ctgtcctaag ccgaactgtg gctgcaccat ct 42

 <210> 66
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:2dVLMiBot
 primer

<400> 66
 agatggtgca gccacagttc ggcttaggac agtcagtttg gt 42

<210> 67
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:TTCL3' Xba
 primer

<400> 67
 cgatctagaa ttaacactct cccctg 26

<210> 68
 <211> 138
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:light chain
 chimeric construct PCR reaction MT-VENT

<220>
 <221> CDS
 <222> (17)..(88)
 <223> V5 epitope and polyhistidine region

<400> 68
 tagagggccc ttcgaaggta agcctatccc taaccctctc ctcggtctcg attctacgcg 60
 taccggtcat catcaccatc accattgagt ttaaaccgcg tgatcagcct cgactgtgcc 120
 ttctaaggcc tgagctcg 138

<210> 69
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial
 Sequence:2dvL_S48G_pMTBip primer

<400> 69
 cacctattag accagtgaat aaatg 25

<210> 70
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial
 Sequence:S48G_N53C_pMTBip primer

<400> 70
 cggttattac aaccacctat tagaccagtg aataaatg 38

<210> 71
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial
Sequence:2dvLKBglII_pMTBip primer

<400> 71
gctcgggaga tgtgctgttg tg

22

<210> 72
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:flexible linker

<400> 72
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10